VISUALIZING METAGENOMIC DATA, Richard J Schmidt, C. Putonti*, Loyola University Chicago, Department of Bioinformatics, Chicago, IL 60660, cputonti@luc.edu

Due to advances in sequencing technologies, it is now possible to sequence the organisms present within individual ecological niches. Such information can provide not only a sense of the species present but also the complex interactions between these organisms. Such studies conducted to date include the human gut, ocean waters, soil, and an old acid mine, just to name a few. The sequencing of such communities, or the compilation of the communities metagenome, has created expansive data sets. Before any biological inference can be made about a community, the billions of sequences synthesized need to be stored, tagged, and analyzed. Multiple software tools have been created to take both a biological and a statistical approach to comparing the data. A key challenge for such tools is providing a means of displaying the data such that biologists can easily interpret it.

The purpose of my research is to design an application to interface with this data in biologically meaningful ways. The primary objective has been to design a Graphical User Interface that is intuitive to the user. This is to be accomplished using the Mac OS X development environment and technologies. The application is being built using modern OS X drawing technologies such as Quartz and Core Animation where appropriate and openGL when high performance of large data sets is required. This has necessitated exploring different ways to gather and present the data to the user and experimenting with usability and smaller data sets. Moreover, the application under development has the capability to query NCBI's GenBank data collection as well as perform analysis on sequences with respect to their nucleotide composition. While still under development, the prototype application will be presented.